

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2008, 16:09:37 ; Search time 15127 Seconds
(without alignments)
11364.178 Million cell updates/sec

Title: US-10-720-177-1
Perfect score: 2100
Sequence: 1 cacaaaatccggcgcaatcca.....ttgggattaagtgcctgcag 2100

Scoring table: IDENTITY_NUC ←
Gapop 10.0 , Gapext 0.1 ←

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_pat:*
3: gb_ph:*
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16: gb_htg2:*

2	2100	100.0	2100	2	DD028154	DD028154 Method fo
c 3	2018.2	96.1	110000	14	BA000036_26	Continuation (27 o
c 4	2018.2	96.1	349136	14	BX927155	BX927155 Corynebac
c 5	2018.2	96.1	349980	2	AX127151	AX127151 Sequence
c 6	1977.9	94.2	110000	14	AP009044_26	Continuation (27 o
7	1589.1	75.7	1629	2	BD164926	BD164926 Novel pol
8	1589.1	75.7	1629	2	AX122809	AX122809 Sequence
9	1436.1	68.4	1468	2	AX764345	AX764345 Sequence
10	1436.1	68.4	1468	2	EA032755	EA032755 Sequence
c 11	884.2	42.1	110000	14	BA000035_25	Continuation (26 o
12	845	40.2	861	2	DD097361	DD097361 CORYNEBAC
13	845	40.2	861	2	DD097362	DD097362 CORYNEBAC
14	845	40.2	861	2	AX063819	AX063819 Sequence
15	845	40.2	861	2	AX063821	AX063821 Sequence
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c 17	415.6	19.8	453	2	AX122808	AX122808 Sequence
18	371.1	17.7	1371	14	DQ019448	DQ019448 Micrococc
19	371.1	17.7	1380	2	E17152	E17152 Micrococcus
20	303.4	14.4	1395	4	AY702086	AY702086 Aspergill
21	303.4	14.4	110000	4	AP007175_15	Continuation (16 o
c 22	296.7	14.1	110000	14	CP000431_73	Continuation (74 o
23	288.8	13.8	110000	14	CP000656_24	Continuation (25 o
c 24	288.5	13.7	110000	14	CP000781_17	Continuation (18 o
c 25	282.5	13.5	110000	14	BA000040_53	Continuation (54 o
c 26	277.6	13.2	110000	14	BA000040_43	Continuation (44 o
c 27	274	13.0	110000	14	CP000454_44	Continuation (45 o
c 28	263.4	12.5	110000	14	CU234118_33	Continuation (34 o
29	249.1	11.9	110000	14	CP000781_13	Continuation (14 o
30	248.9	11.9	1368	2	AR319163	AR319163 Sequence
c 31	245.5	11.7	110000	14	CP000494_37	Continuation (38 o
32	244.1	11.6	110000	14	CP000521_11	Continuation (12 o
33	234.1	11.1	110000	14	CR543861_10	Continuation (11 o
34	220	10.5	110000	14	CP000473_005	Continuation (6 of
35	209.2	10.0	110000	14	CP000474_03	Continuation (4 of
c 36	205.9	9.8	110000	14	CP000325_38	Continuation (39 o
37	203.4	9.7	110000	14	AM711867_00	AM711867 Clavibact
38	196.2	9.3	110000	14	CP000449_31	Continuation (32 o
39	194.8	9.3	110000	14	CP000353_01	Continuation (2 of
40	188.3	9.0	110000	14	CP000117_11	Continuation (12 o
c 41	178.6	8.5	110000	14	CP000473_067	Continuation (68 o
c 42	175.5	8.4	110000	14	BA000019_35	Continuation (36 o
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c 44	172.1	8.2	110000	14	BX571966_08	Continuation (9 of
c 45	172.1	8.2	110000	14	CP000011_08	Continuation (9 of

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
CQ817719
LOCUS CQ817719 2100 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 1 from Patent EP1424397.
ACCESSION CQ817719
VERSION CQ817719.1 GI:48426722
KEYWORDS .
SOURCE Brevibacterium flavum

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	2100	100.0	2100	2	CQ817719		CQ817719 Sequence

Qy	61	TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATAGAAATAGCGCTTGTGCAGCCACCC	120
Db	28439	TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATAGAAATAGCGCTTGTGCAGCCACCC--	28382
Qy	121	ACTCTCAACGGCAGCC-----GCCAGCGCTGGCATCAGCCAGGATTTAT	166
Db	28381	---CTCAACGGCAGCCGCCAGCGAGCCTGTGCCAGCGCTGGCATCAGCCAGGATTTAT	28325
Qy	167	TAGGACCGGCGATATAGGTAATGGATGGCACCCTGATCCACCAATGCACACAGCCT	226
Db	28324	TAGGACCGGCGATATAGGTAATGGAGCGGACCCCTGATCCACCAATGCACACAGCCT	28265
Qy	227	TCGCCGTACCGTCGTAGTTATCCACCATCAGCTGGGAATACCTTGCACTTCACGGCTCA	286
Db	28264	TGCGGCGACCCGTCGTAGTTATCCACCATCAGCTGGGAATACCTTGCACTTCACGGCTCA	28205
Qy	287	TTAATACAGTGGGAATTTCCCGCGGACTTTGTGGATCTCCACAGAATCCATCCTTGAAG	346
Db	28204	TTAATACAGTGGGAATTTCCCGCGGACTTTGTGGATCTCCACAGAATCCATCCTTGAAG	28145
Qy	347	CAGCGAGCAATAAGCCATCGCGTGGGGGACGATCTTGTCCAGCACTCCCTGGACTTAA	406
Db	28144	CAGCGAGCAATAAGCCATCGCGTGGGGGACGATCTTGTCCAGCACTCCCTGGACTTAA	28085
Qy	407	TCGCCGACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCCTGCGGATGCT	466
Db	28084	TCGCCGACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCCTGCGGCGTGT	28025
Qy	467	GCGCGCCCTGGAATAATCCAGAAGAAGGATTCGATGCATCGGTGGCAACCATACGGA	526
Db	28024	GCGCGCCCGGGAATAATCCAGAAGAAGGATTCGAGCGATCGGCGGCAACCATACGGA	27965
Qy	527	TGATACCGGTGTTTGGCGCTGAAAGCCTGAGTTTCCACACGCGTTGCGGATTTTCTCC	586
Db	27964	TGAGGCCGGTGTTTGGCGCTGAAAGCCTGAGTTTCCACACGCGTTGCGGATTTTCTCC	27905
Qy	587	GCAGTGGAAAACTCACTCGCCAGGCTGCGAAAACGCCCGGACACAGTGGAAAGGGAG	646
Db	27904	GCAGTGGAAAACTCACTCGCCAGGCTGCGAAAACGCCCGGACACAGTGGAAAGGGAG	27845
Qy	647	ACGCCAGCGACTTTTGGGACATCAATAATGGTGGCTTTTGGTCTGTG-GCCCGAGAA	705
Db	27844	ACGCCAGCGACTTTTGGGACATCAATAATGGTGGCTTTTGGTCTGTGAGAGCCCGAGAA	27785
Qy	706	TCTGTCATGCACAAGAGTATATAGCGCAAAGAAATCACTAGTCTTGATTCTATGTTGAC	765
Db	27784	TCTGTCATGCACAAGAGTATATAGCGCAAAGAAATCACTAGTCTTGATTCTATGTTGAC	27725
Qy	766	GATGCCGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCGCGACACCACTCCGG	825
Db	27724	GATGCCGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCGCGACACCACTCCGG	27665
Qy	826	CGAGTTGGCGGATTACATCCCGGAACATAAATCTGCCGACCCAAACCCGCTGGCAGTAGC	885
Db	27664	CGAGTTGGCGGATTACATCCCGGAACATAAATCTGCCGACCCAAACCCGCTGGCAGTAGC	27605

Fragment Name	Begin	End
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BA000036_02	200001	310000
BA000036_03	300001	410000
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BA000036_09	900001	1010000
BA000036_10	1000001	1110000
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BA000036_30	3000001	3110000
BA000036_31	3100001	3210000
BA000036_32	3200001	3309494

Qy 1 CACAAAATCCGGGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAAATGCCTCAT 60
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Db 28499 CACAAAATCCGGGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAAATGCCTCAT 28440

Qy 886 CCTGTGCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCAT 945
 Db 27604 CCTGTGCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCAT 27545

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Qy 1006 GGTCTCTGCATCCGTGGCCTTGAACCCCTCCGGTGAGGCTTCAACGAATTTCCCTCGA 1065
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Qy 1066 CGCGGAAAAACGCCCCATGAACCCCATGATCAACGCCGCGCGATCGCCATCAACCAGCT 1125
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Qy 1126 GATCAACGGCTCCGACTCCACCGTGAAGACCGAGTGAAAAAATCCGACACTACTTCTC 1185
 Db 27364 GATCAACGGCTCCGATTCACCGTGAAGACCGCGTAAAAAATCCGACACTACTTCTC 27305

Qy 1186 TGAAGTTGCTGGACGCGAACTCACCATCGACGCGGTGCTTGGCAATCCGAATCGCCGG 1245
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Qy 1246 CGCCGACCGCAACCTCTCCATCGCCCATGCTGCGCACTATGGCGTCATGAAGACGA 1305
 Db 27244 CGCCGACCGCAACCTCTCCATCGCCCATGCTGCGCAATACGGCGTCATGAAGACGA 27185

Qy 1306 AGCCCACGACGCCGCTCTCAGCTACACGCTGCAATGTGCCATCAAAGTAACACGCGCGA 1365
 Db 27184 AGCCCACGACGCCGCTCTCAGCTACACGCTGCAATGTGCCATCAAAGTAACACGCGCGA 27125

Qy 1366 CCTCGCAGTCATGACCGCCACGCTCGCCCGCGCGGCACGACCAATTACCGCAAGAA 1425
 Db 27124 CCTCGCAGTCATGACCGCCACGCTCGCCCGCGCGGCACGACCAATTACCGCAAGAA 27065

Qy 1426 GCTTCTCGACGCCCGGCTCTGCCGCTCACCTCTCCGTATGGCTTCAGCAGGCATGTA 1485
 Db 27064 GCTTCTCGACGCCCGGCTCTGCCGCTCACCTCTCCGTATGGCTTCAGCAGGCATGTA 27005

Qy 1486 CGACGAGGCGAGGCGAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGG 1545
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Qy 1546 CGGACTCATCGGCATTCTGCCAGGTGAGTGGGCTCGCCACATTTTCCCGACGCTGAA 1605
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Qy 1606 CCCCAGAGCAACAGCGTGCAGCGCGTAAAAATATTCAGACAGCTTTCCGACGACATGGG 1665
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Qy 1846 AGTACTTAGCTTCCACCCCGTAGCCATCCGCATGATCAAAGAAGGCCCTCAAACGCATCCG 1905
 Db 26644 AGTACTTAGCTTCCACCCCGTAGCCATCCGCATGATCAAAGAAGGCCCTCAAACGCATCCG 26585

Qy 1906 CGACGAGGCTTTGAGGTGTTTCATCCTCGACCCAGATGACGACTGCCCCGATTTCATGTT 1965
 Db 26584 CGACGAGGCTTTGAGGTGTTTCATCCTCGACCCAGATGACGACTGCCCCGATTTCATGTT 26525

Qy 1966 TTCCGACGCGACCATCTGCAAGAAGACGAGTGTGACCGGTAGCTTTTGGTCTGAACAATT 2025
 Db 26524 TTCCGACGCGACCATCTGCAAGAAGACGAGTGTGACCGGTAGCTTTTGGTCTGAACAATT 26465

Qy 2026 CGAAGGAGATTAATCGGTGAAAAAGAAGCTTATGTTGCCCTTTGATTGTTGCAGCTTTGGG 2085
 Db 26464 CTAAGGAGATTAATCGGTGAAAAAGAAGCTTATGTTGCCCTTTGATTGTTGCAGCTTTGGG 26405

Qy 2086 ATTAAGTGCCTGCAG 2100
 Db 26404 GTTAAGTGCCTGCAG 26390

RESULT 4
 BX927155/c

LOCUS BX927155 349136 bp DNA linear BCT 14-NOV-2006

DEFINITION *Corynebacterium glutamicum* ATCC 13032, IS fingerprint type 4-5, complete genome; segment 8/10.

ACCESSION BX927155 BX927147

VERSION BX927155.1 GI:41326514

KEYWORDS complete genome.

SOURCE *Corynebacterium glutamicum* ATCC 13032
 ORGANISM *Corynebacterium glutamicum* ATCC 13032
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE 1 (bases 1 to 349136)

AUTHORS Kalinowski,J., Bathe,B., Bartels,D., Bischoff,N., Bott,M., Burkovski,A., Dusch,N., Eggeling,L., Eikmanns,B.J., Gaigalat,L., Goesmann,A., Hartmann,M., Huthmacher,K., Kramer,R., Linke,B., McHardy,A.C., Meyer,F., Mockel,B., Pfefferle,W., Puhler,A., Rey,D.A., Ruckert,C., Rupp,O., Sahn,H., Wendisch,V.F., Wiegrabe,I. and Tauch,A.

TITLE The complete *Corynebacterium glutamicum* ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins

JOURNAL J. Biotechnol. 104 (1-3), 5-25 (2003)

PUBMED 12948626

REFERENCE 2 (bases 1 to 349136)

AUTHORS Kalinowski,J.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,